

>AF328296 ACCESSION:AF328296 NID: gi 13957726 gb AF328296.1 AF328296

Homo sapiens myopalladin mRNA, complete cds

Length = 5707

Score = 2649 bits (6790), Expect = 0.0

Identities = 1312/1320 (99%), Positives = 1312/1320 (99%), Gaps = 6/1320 (0%)

Frame = +2

Query: 1 MQDDSI EASTSISQLLRESYLAETRHRGN NERSRAEPSSNPCHFGSPSGAAEGGGGQDDL 60
Sbjct: 488 MQDDSI EASTSISQLLRESYLAETRHRGN NERSRAEPSSNPCHFGSPSGAAEGGGGQDDL 667

Query: 61 PDL SAFLSQEELDES VN LARLAINYDPLEKADETQARKRLSPDQMKHSPNLSFEPNFCQD 120
Sbjct: 668 PDL SAFLSQEELDES VN LARLAINYDPLEKADETQARKRLSPDQMKHSPNLSFEPNFCQD 847

Query: 121 NPRSPTSSKES PQEAKRPQY CSETQSKKVFLNKAADFIEELSSLFKSHSSKRIRPRACKN 180
Sbjct: 848 NPRSPTSSKES PQEAKRPQY CSETQSKKVFLNKAADFIEELSSLFKSHSSKRIRPRACKN 1027

Query: 181 HKSKLESQNKVMQENSSSFSDLSE RRRSSVPIPIPADTRDNEVNHAEQQEAKRREAEQ 240
Sbjct: 1028 HKSKLESQNKVMQENSSSFSDLSE RRRSSVPIPIPADTRDNEVNHAEQQEAKRREAEQ 1207

Query: 241 AASEAAGGDTTPGSSPSSLYEEPLGQPPRFTQKLR SREVPEGTRVQLDCIVVGIPPPQV 300
Sbjct: 1208 AASEAAGGDTTPGSSPSSLYEEPLGQPPRFTQKLR SREVPEGTRVQLDCIVVGIPPPQV 1387

Query: 301 RWYCEGKELENSPDIHIVQAGNLHSLTIAEAFEEDTGRYSCFASNIYGT DSTSAEIYIEG 360
Sbjct: 1388 RWYCEGKELENSPDIHIVQAGNLHSLTIAEAFEEDTGRYSCFASNIYGT DSTSAEIYIEG 1567

Query: 361 VSSSDSEGDPNKEEMNRIQKPNEVSSPPTTS AVIPPAVPQAQHLVAQPRVATIQQCQSPT 420
Sbjct: 1568 VSSSDSEGDPNKEEMNRIQKPNEVSSPPTTS AVIPPAVPQAQHLVAQPRVATIQQCQSPT 1747

Query: 421 NYLQGLDGKPIIAAPVFTKMLQNL SASEGQLVVFECRVKGAPSPKVEWYREGTLIEDSPD 480
Sbjct: 1748 NYLQGLDGKPIIAAPVFTKMLQNL SASEGQLVVFECRVKGAPSPKVEWYREGTLIEDSPD 1927

Query: 481 FRILQKKPRSMAEPEEICTLVIAEVFAEDSGCFTCTASNKYGT VSSIAQLHVRGNEDLSN 540
Sbjct: 1928 FRILQKKPRSMAEPEEICTLVIAEVFAEDSGCFTCTASNKYGT VSSIAQLHVRGNEDLSN 2107

Query: 541 NGSLHSAN-TTNLAAIEPQSPPHSEPPSVEQPPKPKLEGVLVNHNEPRSSSRIGLRVHF 599
Sbjct: 2108 NGSLHSAN-TTNLAAIEPQSPPHSEPPSVEQPPKPKLEGVLVNHNEPRSSSRIGLRVHF 2287

Query: 600 NLPEDDKGSEASSEAGVVTTRQTRPDS-QERFNGQATKTPEPSFPVKEPPPV LAKPKLDS 658
Sbjct: 2288 NLPEDDKGSEASSEAGVVTTRQTRPDS-QERFNGQATKTPEPSFPVKEPPPV LAKPKLDS 2467

Query: 659 TQLQQ LHNQVLLEQHQLQNPPPS SPKEFPF-MTVLNSNAPPAVTTS-KQVKAPSSQTFSL 716
Sbjct: 2468 TQLQQ LHNQVLLEQHQLQNPPPS SPKEFPF-MTVLNSNAPPAVTTS-KQVKAPSSQTFSL 2647

Query: 717 ARPKYFFPSTNTTAATVAPSSSPVFTLSSTPQTIQRTVSKESSLVSHPSVQTKSPGGLSI 776
 ARPKYFFPSTNTTAATVAPSSSPVFTLSSTPQTIQRTVSKESSLVSHPSVQTKSPGGLSI
 Sbjct: 2648 ARPKYFFPSTNTTAATVAPSSSPVFTLSSTPQTIQRTVSKESSLVSHPSVQTKSPGGLSI 2827

Query: 777 QNEPLPPGPTE-TPPPFTFSIPSGNQFQPRCVSIPVVSPTSRIQNPVAFLLSSVLPSPAI 835
 QNEPLPPGPTE TPPPFTFSIP GNQFQPRCVSIPVVSPTSRIQNPVAFLLSSVLPSPAI
 Sbjct: 2828 QNEPLPPGPTEPTPPPFTFSIPRGNQFQPRCVSIPVVSPTSRIQNPVAFLLSSVLPSPAI 3007

Query: 836 PPTNAM-LPRSAPSMPSQGLAKKNTKSPQPVNDDNIRETKNAVIRDLGKKITFSDVRPNQ 894
 PPTNAM LPRSAPSMPSQGLAKKNTKSPQPVNDDNIRETKNAVIRDLGKKITFSDVRPNQ
 Sbjct: 3008 PPTNAMGLPRSAPSMPSQGLAKKNTKSPQPVNDDNIRETKNAVIRDLGKKITFSDVRPNQ 3187

Query: 895 QEYKISSFEQRLMNEIEFRLERTPVDESDDDEIQHDEIPTGKCIAPIFDKRLKHFRVTEGS 954
 QEYKISSFEQRLMNEIEFRLERTPVDESDDDEIQHDEIPTGKCIAPIFDKRLKHFRVTEGS
 Sbjct: 3188 QEYKISSFEQRLMNEIEFRLERTPVDESDDDEIQHDEIPTGKCIAPIFDKRLKHFRVTEGS 3367

Query: 955 PVTFTCKIVGIPVPKVYWFKDQKQISKRNEHCKMRREGDGTCSLHIESTTSDDDGNYTIM 1014
 PVTFTCKIVGIPVPKVYWFKDQKQISKRNEHCKMRREGDGTCSLHIESTTSDDDGNYTIM
 Sbjct: 3368 PVTFTCKIVGIPVPKVYWFKDQKQISKRNEHCKMRREGDGTCSLHIESTTSDDDGNYTIM 3547

Query: 1015 AANPQGRISCSGHLMVQSLPIRSRLTSAGQSHRGRSRVQERDKEPLQERFFRPHFLQAPG 1074
 AANPQGRISCSGHLMVQSLPIRSRLTSAGQSHRGRSRVQERDKEPLQERFFRPHFLQAPG
 Sbjct: 3548 AANPQGRISCSGHLMVQSLPIRSRLTSAGQSHRGRSRVQERDKEPLQERFFRPHFLQAPG 3727

Query: 1075 DMVAHEGRLCRLDCKVSGLPPPELTWLLNGQPVLDPASHKMLVRETGVHSLLDPLTQRD 1134
 DMVAHEGRLCRLDCKVSGLPPPELTWLLNGQPVLDPASHKMLVRETGVHSLLDPLTQRD
 Sbjct: 3728 DMVAHEGRLCRLDCKVSGLPPPELTWLLNGQPVLDPASHKMLVRETGVHSLLDPLTQRD 3907

Query: 1135 AGTYKCIATNKTGQNSFSLELSVVAKEVKKAPVILEKLQNCVPEGHPVRLECRVIGMPP 1194
 AGTYKCIATNKTGQNSFSLELSVVAKEVKKAPVILEKLQNCVPEGHPVRLECRVIGMPP
 Sbjct: 3908 AGTYKCIATNKTGQNSFSLELSVVAKEVKKAPVILEKLQNCVPEGHPVRLECRVIGMPP 4087

Query: 1195 PVFYWKDNETIPCTRERISMHQDTTGYACLLIQPAKKS DAGWYTL SAKNEAGIVSCTAR 1254
 PVFYWKDNETIPCTRERISMHQDTTGYACLLIQPAKKS DAGWYTL SAKNEAGIVSCTAR
 Sbjct: 4088 PVFYWKDNETIPCTRERISMHQDTTGYACLLIQPAKKS DAGWYTL SAKNEAGIVSCTAR 4267

Query: 1255 LDIYAQWHHQIPPPMSVRPSGSRYSLSKGLDIFSAFSSMESTMVYSCSSRSVVEDEL 1314
 LDIYAQWHHQIPPPMSVRPSGSRYSLSKGLDIFSAFSSMESTMVYSCSSRSVVEDEL
 Sbjct: 4268 LDIYAQWHHQIPPPMSVRPSGSRYSLSKGLDIFSAFSSMESTMVYSCSSRSVVEDEL 4447